

SEQUENCE LISTING

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<120> A Process for Preparing L-Threonione

<130> 7601/88025

<140> 10/567749

<141> 2006-02-10

<160> 10

<170> PatentIn version 3.4

<210> 1

<211> 993

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(990)

<223> rpos gene

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ttt gat gag aac gga gtt gag gtt ttt gac gaa aag gcc tta gta gaa	96
Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu	
20 25 30	

cag gaa ccc agt gat aac gat ttg gcc gaa gag gaa ctg tta tcg cag	144
Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln	
35 40 45	

gga gcc aca cag cgt gtg ttg gac gcg act cag ctt tac ctt ggt gag	192
Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu	
50 55 60	

att ggt tat tca cca ctg tta acg gcc gaa gaa gaa gtt tat ttt gcg	240
Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala	
65 70 75 80	

cgt cgc gca ctg cgt gga gat gtc gcc tct cgc cgc cgg atg atc gag	288
Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu	
85 90 95	

agt aac ttg cgt ctg gtg gta aaa att gcc cgc cgt tat ggc aat cgt	336
Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg	
100 105 110	

ggt ctg gcg ttg ctg gac ctt atc gaa gag ggc aac ctg ggg ctg atc	384
Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile	
115 120 125	

cgc gcg gta gag aag ttt gac ccg gaa cgt ggt ttc cgc ttc tca aca	432
Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr	
130 135 140	
tac gca acc tgg tgg att cgc cag acg att gaa cgg gcg att atg aac	480
Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn	
145 150 155 160	
caa acc cgt act att cgt ttg ccg att cac atc gta aag gag ctg aac	528
Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn	
165 170 175	
gtt tac ctg cga acc gca cgt gag ttg tcc cat aag ctg gac cat gaa	576
Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu	
180 185 190	
cca agt gcg gaa gag atc gca gag caa ctg gat aag cca gtt gat gac	624
Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp	
195 200 205	
gtc agc cgt atg ctt cgt ctt aac gag cgc att acc tcg gta gac acc	672
Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr	
210 215 220	
ccg ctg ggt ggt gat tcc gaa aaa gcg ttg ctg gac atc ctg gcc gat	720
Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp	
225 230 235 240	
gaa aaa gag aac ggt ccg gaa gat acc acg caa gat gac gat atg aag	768
Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys	
245 250 255	
cag agc atc gtc aaa tgg ctg ttc gag ctg aac gcc aaa cag cgt gaa	816
Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu	
260 265 270	
gtg ctg gca cgt cga ttc ggt ttg ctg ggg tac gaa gcg gca aca ctg	864
Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu	
275 280 285	
gaa gat gta ggt cgt gaa att ggc ctc acc cgt gaa cgt gtt cgc cag	912
Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln	
290 295 300	
att cag gtt gaa ggc ctg cgc cgt ttg cgc gaa atc ctg caa acg cag	960
Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln	
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ggg ctg aat atc gaa gcg ctg ttc cgc gag taa	993
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325

330

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<213> Escherichia coli

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Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln			
35	40	45	
Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu			
50	55	60	
Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala			
65	70	75	80
Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu			
85	90	95	
Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg			
100	105	110	
Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile			
115	120	125	
Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr			
130	135	140	
Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn			
145	150	155	160
Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn			
165	170	175	
Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu			
180	185	190	
Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp			
195	200	205	
Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr			
210	215	220	
Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp			
225	230	235	240
Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys			
245	250	255	
Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu			
260	265	270	
Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu			
275	280	285	
Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln			
290	295	300	
Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln			
305	310	315	320
Gly Leu Asn Ile Glu Ala Leu Phe Arg Glu			
325	330		

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 <213> Escherichia coli

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 <222> (1)..(990)
 <223> rpoS allele

<220>
 <221> misc_feature
 <222> (97)..(99)
 <223> amber codon

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 gccgaagagg aactgttata gcagggagcc acacagcgtg tgttggaagc gactcagctt 180
 taccttggtg agattgggta ttcaccactg ttaacggccg aagaagaagt ttatattgag 240
 cgtcgcgcac tgcgtggaga tgcgcctct cgcgcgga tgatcgagag taacttgcgt 300
 ctggtggtaa aaattgcccg ccgttatggc aatcgtggtc tggcggttgc ggaccttata 360
 gaagagggca acctggggct gatccgcgcg gtagagaagt ttgaccgga acgtgggttc 420
 cgcttctcaa catacgcaac ctggtggatt cgccagacga ttgaacgggc gattatgaac 480
 caaaccgta ctattcggtt gccgattcac atcgtaaagg agctgaacgt ttacctgcga 540
 accgcacgtg agttgtccca taagctggac catgaaccaa gtgcggaaga gatcgagag 600
 caactggata agccagttga tgacgtcagc cgtatgcttc gtcttaacga gcgcattacc 660
 tcggtagaca ccccgctggg tggtagattc gaaaaagcgt tgctggacat cctggccgat 720
 gaaaaagaga acggtccgga agataccacg caagatgacg atatgaagca gagcatcgtc 780
 aaatggctgt tcgagctgaa cgccaaacag cgtgaagtgc tggcacgtcg attcggttg 840
 ctggggtacg aagcggcaac actggaagat gtaggtcgtg aaattggcct caccgtgaa 900
 cgtgttcgcc agattcaggt tgaaggcctg cgcggttgc gcgaaatcct gcaaacgcag 960
 gggctgaata tcgaagcgt gttccgcgag taa 993

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<220>
 <221> tRNA
 <222> (1)..(75)
 <223> supE allele

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 ctcgtacccc agcca 75

<210> 5
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 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1542)
 <223> ilvA-Gen

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 1 5 10 15
 tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg 96
 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
 20 25 30
 ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att 144
 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
 35 40 45
 ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192
 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 50 55 60
 ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240
 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 65 70 75 80
 ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt 288
 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 85 90 95
 tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc 336
 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 100 105 110
 acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg 384
 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
 115 120 125
 ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa 432
 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 130 135 140
 ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg 480
 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 145 150 155 160
 atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag 528
 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
 165 170 175

gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu 180 185 190	576
gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys 195 200 205	624
gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu 210 215 220	672
gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu 225 230 235 240	720
ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln 245 250 255	768
gag tat ctc gac gac atc atc acc gtc gat agc gat gcg atc tgt gcg Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala 260 265 270	816
gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg gaa ccc tct Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser 275 280 285	864
ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn 290 295 300	912
att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn 305 310 315 320	960
ttc cac ggc ctg cgc tac gtc tca gaa cgc tgc gaa ctg ggc gaa cag Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln 325 330 335	1008
cgt gaa gcg ttg ttg gcg gtg acc att ccg gaa gaa aaa ggc agc ttc Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe 340 345 350	1056
ctc aaa ttc tgc caa ctg ctt ggc ggg cgt tcg gtc acc gag ttc aac Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn 355 360 365	1104
tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg 370 375 380	1152
ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn 385 390 395 400	1200
gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys 405 410 415	1248

cta cac gtg cgc tat atg gtc ggc gga cgt cca tgc cat ccg ttg cag 1296
 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
 420 425 430

gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg 1344
 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
 435 440 445

cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac 1392
 Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
 450 455 460

tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa 1440
 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
 465 470 475 480

ctt ggc gac cat gaa ccg gat ttc gaa acc ccg ctg aat gag ctg ggc 1488
 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
 485 490 495

tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg 1536
 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
 500 505 510

gcg ggt tag 1545
 Ala Gly

<210> 6
 <211> 514
 <212> PRT
 <213> Escherichia coli

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Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
 35 40 45

Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 50 55 60

Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 65 70 75 80

Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 85 90 95

Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 100 105 110

Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
 115 120 125

Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 130 135 140

Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 145 150 155 160
 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
 165 170 175
 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu
 180 185 190
 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
 195 200 205
 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
 210 215 220
 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
 225 230 235 240
 Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
 245 250 255
 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
 260 265 270
 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser
 275 280 285
 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn
 290 295 300
 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
 305 310 315 320
 Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln
 325 330 335
 Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe
 340 345 350
 Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn
 355 360 365
 Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
 370 375 380
 Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
 385 390 395 400
 Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
 405 410 415
 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
 420 425 430
 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
 435 440 445
 Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
 450 455 460

Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
465 470 475 480

Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
485 490 495

Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
500 505 510

Ala Gly

<210> 7
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<220>
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<223> ilvA-Allel

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1 5 10 15

tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg 96
Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
20 25 30

ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att 144
Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
35 40 45

ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192
Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
50 55 60

ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240
Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
65 70 75 80

ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt 288
Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
85 90 95

tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc 336
Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
100 105 110

acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg 384
Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
115 120 125

ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa 432

Leu	Leu	His	Gly	Ala	Asn	Phe	Asp	Glu	Ala	Lys	Ala	Lys	Ala	Ile	Glu	
130						135					140					
ctg	tca	cag	cag	cag	ggg	ttc	acc	tgg	gtg	ccg	ccg	ttc	gac	cat	ccg	480
Leu	Ser	Gln	Gln	Gln	Gly	Phe	Thr	Trp	Val	Pro	Pro	Phe	Asp	His	Pro	
145					150					155					160	
atg	gtg	att	gcc	ggg	caa	ggc	acg	ctg	gcg	ctg	gaa	ctg	ctc	cag	cag	528
Met	Val	Ile	Ala	Gly	Gln	Gly	Thr	Leu	Ala	Leu	Glu	Leu	Leu	Gln	Gln	
				165					170					175		
gac	gcc	cat	ctc	gac	cgc	gta	ttt	gtg	cca	gtc	ggc	ggc	ggc	ggg	ctg	576
Asp	Ala	His	Leu	Asp	Arg	Val	Phe	Val	Pro	Val	Gly	Gly	Gly	Gly	Leu	
			180					185					190			
gct	gct	ggc	gtg	gcg	gtg	ctg	atc	aaa	caa	ctg	atg	ccg	caa	atc	aaa	624
Ala	Ala	Gly	Val	Ala	Val	Leu	Ile	Lys	Gln	Leu	Met	Pro	Gln	Ile	Lys	
		195					200					205				
gtg	atc	gcc	gta	gaa	gcg	gaa	gac	tcc	gcc	tgc	ctg	aaa	gca	gcg	ctg	672
Val	Ile	Ala	Val	Glu	Ala	Glu	Asp	Ser	Ala	Cys	Leu	Lys	Ala	Ala	Leu	
	210					215					220					
gat	gcg	ggt	cat	ccg	gtt	gat	ctg	ccg	cgc	gta	ggg	cta	ttt	gct	gaa	720
Asp	Ala	Gly	His	Pro	Val	Asp	Leu	Pro	Arg	Val	Gly	Leu	Phe	Ala	Glu	
225					230					235					240	
ggc	gta	gcg	gta	aaa	cgc	atc	ggt	gac	gaa	acc	ttc	cgt	tta	tgc	cag	768
Gly	Val	Ala	Val	Lys	Arg	Ile	Gly	Asp	Glu	Thr	Phe	Arg	Leu	Cys	Gln	
				245					250					255		
gag	tat	ctc	gac	gac	atc	atc	acc	gtc	gat	agc	gat	gcg	atc	tgt	gcg	816
Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala	
			260					265					270			
gcg	atg	aag	gat	tta	ttc	gaa	gat	gtg	cgc	gcg	gtg	gcg	aaa	ccc	tct	864
Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Lys	Pro	Ser	
		275					280					285				
ggc	gcg	ctg	gcg	ctg	gcg	gga	atg	aaa	aaa	tat	atc	gcc	ctg	cac	aac	912
Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn	
		290				295					300					
att	cgc	ggc	gaa	cgg	ctg	gcg	cat	att	ctt	tcc	ggt	gcc	aac	gtg	aac	960
Ile	Arg	Gly	Glu	Arg	Leu	Ala	His	Ile	Leu	Ser	Gly	Ala	Asn	Val	Asn	
305					310					315					320	
ttc	cac	ggc	ctg	cgc	tac	gtc	tca	gaa	cgc	tgc	gaa	ctg	ggc	gaa	cag	1008
Phe	His	Gly	Leu	Arg	Tyr	Val	Ser	Glu	Arg	Cys	Glu	Leu	Gly	Glu	Gln	
				325					330					335		
cgt	gaa	gcg	ttg	ttg	gcg	gtg	acc	att	ccg	gaa	gaa	aaa	ggc	agc	ttc	1056
Arg	Glu	Ala	Leu	Leu	Ala	Val	Thr	Ile	Pro	Glu	Glu	Lys	Gly	Ser	Phe	
			340					345					350			
ctc	aaa	ttc	tgc	caa	ctg	ctt	ggc	ggg	cgt	tcg	gtc	acc	gag	ttc	aac	1104
Leu	Lys	Phe	Cys	Gln	Leu	Leu	Gly	Gly	Arg	Ser	Val	Thr	Glu	Phe	Asn	
		355					360					365				

tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc	1152
Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg	
370 375 380	
ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac	1200
Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn	
385 390 395 400	
gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag	1248
Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys	
405 410 415	
cta cac gtg cgc tat atg gtc ggc gga cgt cca tcg cat ccg ttg cag	1296
Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln	
420 425 430	
gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg	1344
Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu	
435 440 445	
cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac	1392
Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His	
450 455 460	
tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa	1440
Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu	
465 470 475 480	
ctt ggc gac cat gaa ccg gat ttc gaa acc cgg ctg aat gag ctg ggc	1488
Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly	
485 490 495	
tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg	1536
Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu	
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gcg ggt tag	1545
Ala Gly	

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 35 40 45
 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 50 55 60
 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 65 70 75 80

Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 85 90 95
 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 100 105 110
 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
 115 120 125
 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 130 135 140
 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 145 150 155 160
 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
 165 170 175
 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu
 180 185 190
 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
 195 200 205
 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
 210 215 220
 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
 225 230 235 240
 Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
 245 250 255
 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
 260 265 270
 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Lys Pro Ser
 275 280 285
 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn
 290 295 300
 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
 305 310 315 320
 Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln
 325 330 335
 Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe
 340 345 350
 Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn
 355 360 365
 Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
 370 375 380
 Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
 385 390 395 400

Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
 405 410 415
 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
 420 425 430
 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
 435 440 445
 Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
 450 455 460
 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
 465 470 475 480
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 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
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Ala Gly

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 gagtctgttc aagctgaccg aaacggatca gcgcatcacc attggtctga acctgccttc 180
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 agtgggtggg aaatcgcgcc caagtctgcc ggagcgcacg gacaatgtgc tggctctgccc 360
 gaacagcaac tgtatcagcc atgccgaacc ggtttcatcc agctttgccc tgcgaaaacg 420
 cgccaatgat atcgcgctca aatgcaaata ctgtgaaaaa gagttttccc ataatgtggt 480
 gctggccaat taattgcggt tggtaataaa agtctggctc cctata atg agc cag 535
 Met Ser Gln
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 act ttt tac cgc tgt aat aaa gga gaa atc atg agc aaa act atc gcg 583
 Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys Thr Ile Ala
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 acg gaa aat gca ccg gca gct atc ggt cct tac gta cag ggc gtt gat 631

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Thr	Gly	Glu	Val	Pro	Ala	Asp	Val	Ala	Ala	Gln	Ala	Arg	Gln	Ser	Leu		
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gat	aac	gta	aaa	gcg	atc	gtc	gaa	gcc	gct	ggc	ctg	aaa	gtg	ggc	gac	775	
Asp	Asn	Val	Lys	Ala	Ile	Val	Glu	Ala	Ala	Gly	Leu	Lys	Val	Gly	Asp		
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atc	gtt	aaa	act	acc	gtg	ttt	gta	aaa	gat	ctg	aac	gac	ttc	gca	acc	823	
Ile	Val	Lys	Thr	Thr	Val	Phe	Val	Lys	Asp	Leu	Asn	Asp	Phe	Ala	Thr		
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gta	aac	gcc	act	tac	gaa	gcc	ttc	ttc	acc	gaa	cac	aac	gcc	acc	ttc	871	
Val	Asn	Ala	Thr	Tyr	Glu	Ala	Phe	Phe	Thr	Glu	His	Asn	Ala	Thr	Phe		
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ccg	gca	cgt	tct	tgc	gtt	gaa	gtt	gcc	cgt	ctg	ccg	aaa	gac	gtg	aag	919	
Pro	Ala	Arg	Ser	Cys	Val	Glu	Val	Ala	Arg	Leu	Pro	Lys	Asp	Val	Lys		
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Ile	Glu	Ile	Glu	Ala	Ile	Ala	Val	Arg	Arg								
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Gly	Val	Asp	Leu	Gly	Asn	Met	Ile	Ile	Thr	Ser	Gly	Gln	Ile	Pro	Val	
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Gln	Ser	Leu	Asp	Asn	Val	Lys	Ala	Ile	Val	Glu	Ala	Ala	Gly	Leu	Lys	
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Val	Gly	Asp	Ile	Val	Lys	Thr	Thr	Val	Phe	Val	Lys	Asp	Leu	Asn	Asp	
			85						90					95		
Phe	Ala	Thr	Val	Asn	Ala	Thr	Tyr	Glu	Ala	Phe	Phe	Thr	Glu	His	Asn	
			100					105					110			
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Asp	Val	Lys	Ile	Glu	Ile	Glu	Ala	Ile	Ala	Val	Arg	Arg				
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